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EXAMINER

SMITH, CAROLYN L

ART UNIT

PAPER NUMBER

1631

DATE MAILED: 07/18/2003

14

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary

Application No.

09/954,531

Applicant(s)

WEAVER, ZOE

Examiner

Carolyn L Smith

Art Unit

1631

-- The MAILING DATE of this communication appears in the cover sheet with the correspondence address --
Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 27 May 2003.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1-35 and 37-48 is/are pending in the application.
- 4a) Of the above claim(s) 18-35 and 37-46 is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 1-17, 47 and 48 is/are rejected.
- 7) ☒ Claim(s) 2, 4-8, 10, 15 and 47 is/are objected to.
- 8) ☒ Claim(s) 1-35 and 37-48 are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
- Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
- 11) ☐ The proposed drawing correction filed on _____ is: a) ☐ approved b) ☐ disapproved by the Examiner.
- If approved, corrected drawings are required in reply to this Office action.
- 12) ☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. §§ 119 and 120

- 13) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
2. ☐ Certified copies of the priority documents have been received in Application No. _____.
3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).
- * See the attached detailed Office action for a list of the certified copies not received.
- 14) ☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).
- a) ☐ The translation of the foreign language provisional application has been received.
- 15) ☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

- 1) ☒ Notice of References Cited (PTO-892)
- 2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) ☒ Information Disclosure Statement(s) (PTO-1449) Paper No(s) 6, 9.
- 4) ☒ Interview Summary (PTO-413) Paper No(s). 13.
- 5) ☐ Notice of Informal Patent Application (PTO-152)
- 6) ☒ Other: *See Continuation Sheet*.

Continuation of Attachment(s) 6). Other: Sequence Match Listing (44 pages).

DETAILED ACTION

Applicant's election with traverse of Group I (claims 1-17); sequence elections of SEQ ID NO: 110, 653, 683, 767, 804, 820, 910, 1019, 1040, and 1247; the amendment of claims 1-5, 9, 11-15, 18, 21-24, and 39; the cancellation of claim 36; and the addition of new claims 47-48 in Paper Nos. 11 and 12, filed 5/27/03, are acknowledged. Claims 18-46 are withdrawn from consideration as being drawn to non-elected Groups.

Based on a telephone interview on 2/21/03, Applicant was allowed to elect up to 10 sequences for the sequence election requirement.

Applicant's traversal is on the grounds that Groups I and VI should be combined as the claims are limited to the use of compounds having activity in the screening claims.

Applicant's request to combine Groups I and VI into one invention was found unpersuasive because of the following reasons (summarized from the restriction paper):

First, Applicant presented no argument or reasoning as to why these Groups should be combined. Second, as summarized on page 5 of the Restriction Paper, mailed 1/27/03, Groups I and VI are directed to a process and method that comprise different means and produce different results/goals. Group I identifies agents using putative modulating materials via cell contact which is different from the results of Group VI. Group VI treats and protects an entity from cancer which is a process not found in the Group I. These distinct processes and methods are often separately characterized and published in literature and would add undue search burden if they were examined together. Thus, they are considered distinct invention types for restriction purposes.

Art Unit: 1631

The requirements are still deemed proper and are therefore made FINAL.

Claims herein under examination are 1-5 (amended), 6-8, 9 (amended), 10, 11-15 (amended), 16-17, 47 (new), and 48 (new).

Claim Objections

Claims 2, 4-8, 10, and 47 are objected to due to the inclusion of subject matter which has been non-elected due to a restriction requirement and therefore withdrawn from consideration.

The non-elected subject matter in claims 2, 4-8, 10, and 47 is summarized as follows: Claims 2, 6-8, 10, and 47 contain sequences, such as sequences other than SEQ ID NO: 110, 653, 683, 767, 804, 820, 910, 1019, 1040, and 1247, which are non-elected subject matter. Removal of non-elected subject matter is requested. Claims 4 and 5 are also objected to due to their direct or indirect dependency from claim 2.

Claim 15 is objected to for the following minor informality: Claim 15 recites the phrase "of one of claim 1" which does not make grammatical sense. Correction of this syntactical inadequacy is requested.

Claim Rejections – 35 U.S.C. 112, first paragraph

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

LACK OF WRITTEN DESCRIPTION

Art Unit: 1631

Claims 1-17, 47, and 48 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor, at the time of the invention was filed, had possession of the claimed invention.

The specification discloses SEQ ID NO: 110, 653, 683, 767, 804, 820, 910, 1019, 1040, and 1247 which correspond to nucleic acid sequences. SEQ ID NO: 110, 653, 683, 767, 804, 820, 910, 1019, 1040, and 1247 and their full complements meet the written description provisions of 35 U.S.C. 112, first paragraph. However, due to the open claim language of "containing a gene that corresponds to a polynucleotide" (claim 1) and "comprising a nucleotide sequence corresponding to a gene" (claim 54), these claims encompass sequences which do not meet the written description provision of 35 U.S.C. 112, first paragraph. The specification provides insufficient written description to support the genus encompassed by these claims.

Vas-Cath Inc. v. Mahurkar, 19 USPQ2d 1111, makes clear that "applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession of *the invention*. The invention is, for purposes of the 'written description' inquiry, *whatever is now claimed*." (See page 1117.) The specification does not "clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed." (See Vas-Cath at page 1116.)

With the exception of SEQ ID NO: 110, 653, 683, 767, 804, 820, 910, 1019, 1040, and 1247, the skilled artisan cannot envision the detailed chemical structure of the encompassed polynucleotides and/or proteins, regardless of the complexity or simplicity of the method of isolation. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method for isolating it. The nucleic acid itself is required. See Fiers v. Revel, 25 USPQ2d 1601, 1606 (CAFC 1993) and Amgen Inc. V. Chugai Pharmaceutical Co. Ltd., 18 USPQ2d 1016. In Fiddes v. Baird, 30 USPQ2d 1481, 1483, claims directed to mammalian FGF's were found unpatentable due to lack of written description for the broad class. The specification provided only the bovine sequence.

Finally, University of California v. Eli Lilly and Co., 43 USPQ2d 1398, 1404, 1405 held that:

Art Unit: 1631

...To fulfill the written description requirement, a patent specification must describe an invention and do so in sufficient detail that one skilled in the art can clearly conclude that "the inventor invented the claimed invention." *Lockwood v. American Airlines, Inc.*, 107 F.3d 1565, 1572, 41 USPQ2d 1961, 1966 (1997); *In re Gosteli*, 872 F.2d 1008, 1012, 10 USPQ2d 1614, 1618 (Fed. Cir. 1989) (" [T]he description must clearly allow persons of ordinary skill in the art to recognize that [the inventor] invented what is claimed."). Thus, an applicant complies with the written description requirement "by describing the invention, with all its claimed limitations, not that which makes it obvious," and by using "such descriptive means as words, structures, figures, diagrams, formulas, etc., that set forth the claimed invention." *Lockwood*, 107 F.3d at 1572, 41 USPQ2d at 1966.

Therefore, only SEQ ID NO: 110, 653, 683, 767, 804, 820, 910, 1019, 1040, and 1247 and their full length complements, but not the full breadth of the claims meet the written description provision of 35 USC 112, first paragraph. The species specifically disclosed are not representative of the genus because the genus is highly variant. Applicant is reminded that Vas-Cath makes clear that the written description provision of 35 USC 112 is severable from its enablement provision. (See page 1115.)

Claims Rejected Under 35 U.S.C. § 112, second paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1-17, 47, and 48 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which the applicant regards as the invention.

Claims 1 (line 3) and 48 (line 4) recite the terms "corresponds" and "corresponding", respectively, which are vague and indefinite. It is unclear what criteria and to what extent the sequence must be similar to a gene to be considered to have the "corresponding" attribute. For

Art Unit: 1631

example, a nucleotide sequence corresponding to a gene could be the full-length nucleotide sequence of that gene. In another example the sequence could be a fragment, as a hybridization probe which is a fragment may be considered to correspond to a gene via the usage of such a probe for detection. Another interpretation is that the nucleotide sequence may include a sequence similar to the gene but with modifications made at various nucleotides and several other scenarios. Clarification of the metes and bounds of the instant claims is required. Claims 2-17 and 47 are also rejected due to their direct and indirect dependency from claim 1.

Claims 1 and 48 recite the terms “increased” (line 5 of both claims and line 14 of claim 48), “elevated” (line 6 of both claims; line 12 of claim 1; and line 12 of claim 48), “increase” (line 11 of claim 1 and line 11 of claim 48), “decrease” (line 13 of claim 1 and line 13 of claim 48) which are vague and indefinite. It is unclear what threshold Applicants intend to use for determining if expression is significantly increased, elevated, or decreased as it is well known that while scientific data may be different, it may not be significantly different if variations are caused by fluctuations including experimental processing or measurement error. Clarification of the metes and bounds of these terms is requested. Claims 2-17 and 47 are also rejected due to their direct and indirect dependency from claim 1.

Claims 1 and 48 recite the phrases “cancerous cell over that in a non-cancerous cell” (claim 1 [lines 5-6 and 14] and claim 48 [lines 5 and 14]) and “non-cancerous cell over that in a cancerous cell” (claim 1 [lines 6-7 and 12] and claim 48 [lines 6 and 12]) which is vague and indefinite. Besides their cancerous status, it is unclear in what aspects these cells are related, such as if these cells are from the same or different type of organ tissue as well as the same or different type of organism which would aid in determining test relevancy. Clarification of the

Art Unit: 1631

metes and bounds of these phrases is requested. Claims 2-17 and 47 are also rejected due to their direct and indirect dependency from claim 1.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

Claims 1-17, 47, and 48 are rejected under 35 U.S.C. 102(e)(2) as being anticipated by Young et al. (WO 01/94629).

The applied reference has a common inventor with the instant application. Based upon the earlier effective U.S. filing date of the reference, it constitutes prior art under 35 U.S.C. 102(e). This rejection under 35 U.S.C. 102(e) might be overcome either by a showing under 37 CFR 1.132 that any invention disclosed but not claimed in the reference was derived from the inventor of this application and is thus not the invention “by another,” or by an appropriate showing under 37 CFR 1.131.

Young et al. disclose a process of screening novel drugs using genes, including oncogenes (page 2, lines 12-17). Young et al. disclose using a set of genes whose expression, non-expression, or change (increase or decrease) in expression, are indicative of cancerous or non-cancerous status of a given cell (page 2, lines 22-25). Young et al. disclose sequences of SEQ ID NO: 1-8447 or sequences substantially identical to these sequences, some of which are

Art Unit: 1631

complete or near matches to SEQ ID NO: 110, 653, 683, 767, 804, 820, 910, 1019, 1040, and 1247 of the instant invention (see Sequence match listings and following paragraph). Young et al. disclose using signature gene sets for assaying the ability of chemical agents to modulate expression of the gene sets up or down (page 3, first paragraph). Young et al. disclose using gene sequences expressed only in infiltrating ductal carcinoma of the breast, only in breast carcinoma, only in normal breast tissues, and only in infiltrating lobular carcinoma of the breast (page 17, third paragraph to page 18, first paragraph). Young et al. disclose using chemical agents known for their ability to modulate cancerous genes (page 3, paragraphs 3 and 4). Young et al. disclose producing a product including collected data with respect to the agent used in the screening process (page 5, first paragraph). Young et al. disclose identifying genes that are expressed at higher levels in cancer cells than in normal cells or expressed at lower levels in cancer cells than in normal cells (page 6, second paragraph). Young et al. disclose exposing cells to chemical agents, determining changes in expression wherein a change is indicative of anti-neoplastic activity (page 6, third paragraph). Young et al. disclose comparing chemical agent exposure versus no exposure to the genes (page 7, first paragraph). Young et al. disclose the chemical agent modulates expression in one, two, three, five, or ten genes, or where all genes are modulated (page 7, second paragraph). Young et al. disclose the agent can be an apoptosis-inducing agent (in claim 21) inducing cell death (page 27, third paragraph). Young et al. disclose in claim 24 the gene number increases which is replication.

Due to the open claim language of “a gene that corresponds to a polynucleotide” (claim 1) and “a polynucleotide comprising a nucleotide sequence corresponding to a gene” (claim 48), a prior art polynucleotide need not be 100% identical, although most of those described below

Art Unit: 1631

are an exact match. Young et al. disclose sequences (ABL62840 and ABL63054) which are 100% identical to SEQ ID NO: 110 of the instant invention. Young et al. disclose sequences (ABL63383, ABL64857, ABL65548, and ABL66020) which are 100% identical to SEQ ID NO: 653 of the instant invention. Young et al. disclose sequences (ABL63413 and ABL63830) which are 100% identical to SEQ ID NO: 683 of the instant invention. Young et al. disclose sequences (ABL63497 and ABL63936) which are 100% identical to SEQ ID NO: 767 of the instant invention. Young et al. disclose sequences (ABL61767 and ABL63534) which are 99.8% identical to SEQ ID NO: 804 of the instant invention. Young et al. disclose a sequence (ABL63550) which is 100% identical to SEQ ID NO: 820 of the instant invention. Young et al. disclose a sequence (ABL63640) which is 97.9% identical to SEQ ID NO: 910 of the instant invention. Young et al. disclose sequences (ABL63749) which are 99.6% identical to SEQ ID NO: 1019 of the instant invention. Young et al. disclose sequences (ABL63770, ABL66331, and ABL67711) which are 100% identical to SEQ ID NO: 1040 of the instant invention. Young et al. disclose a sequence (ABL63977) which is 99.8% identical to SEQ ID NO: 1247 of the instant invention.

Thus, Young et al. anticipate the instant invention.

Claim Rejections – 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary

Art Unit: 1631

skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

Claims 1-17, 47, and 48 are rejected under 35 U.S.C. 103(a) as being unpatentable over Robinson et al. (P/N 6,232,065) in view of GenBank (various Accession numbers), Young et al. (WO 01/94629), and Kinzler et al. (P/N 5,702,903).

Robinson et al. describe methods and compositions for screening factors that affect the expression patterns of individual genes or groups of genes in various disease states such as from normal, cancer, and other metastatic tissue samples (col. 1, lines 4-10; col. 12, lines 17-44; and col. 23, lines 12-38). Robinson et al. describe studying the effects of exogenously added compounds (col. 22, lines 59-62) on thousands of genes including multiple genes from specific gene families (col. 13, lines 1-22) which is reasonably interpreted as a signature gene set.

Robinson et al. describe comparing metastatic cancer tissue with non-metastatic cancer tissue to identify differentially expressed genes as markers of metastatic potential (col. 16, lines 19-22).

The presence or absence of these markers can then be assessed in various clinical cancer isolates (col. 16, lines 22-24). Robinson et al. describe anti-cancer compounds (col. 16, line 31) and drug screening to look for compounds to alter genes known to be implicated in a disease state, such as gene over-expression or under-expression in cancer cells as opposed to normal cells (col. 16, lines 48-57). Robinson et al. provide an assaying example such that if a gene family member is known to be overexpressed in cancer cells (compared to normal cells), then one can look for drugs that reduce the expression of the suspect gene to normal levels (col. 16, lines 52-57).

Robinson et al. describe variations of such comparisons are included in their invention (col. 16, lines 58-60). Robinson et al. describe examining an entire gene family expression profile and

Art Unit: 1631

identifying important marker genes that can be used in future experiments to identify cancer and other cancer-related testing (col. 17, lines 4-19). Robinson et al. describe providing results for gene expression levels. Robinson et al. describe results being presented in a comparative format including high expression in most samples, low expression in most samples, and expression limited to only a few cell types in the panel (col. 20, lines 48-58) which exemplifies various degrees of expression. Robinson et al. describe many of the multiple genes showing expression changes in a particular tyrosine kinase gene family set (col. 21, lines 9-27 and col. 23, lines 12-38) as mentioned in claims 47-49. Robinson et al. describe using an assortment of tissues from various organs, including from a breast adenocarcinoma cell line (col. 19, line 63 and Table 1). Robinson et al. describe using adenocarcinoma cell lines, glioblastoma, and neuroblastoma cells in Table 1. Robinson et al. describe various gene modulating compounds such as drugs, growth factors, cytokines, and hormones that can affect neoplastic activity of cancerous cells upon contact (col. 22, lines 59-67). Robinson et al. describe an increased concentration of cancerous cells which is an accelerated replication compared to normal cells (col. 23, lines 28-38). Robinson et al. do not describe a decrease in neoplastic activity due to cell death and particular sequences (SEQ ID NO: 110, 653, 683, 767, 804, 820, 910, 1019, 1040, and 1247) that are elected in the instant invention.

Young et al. describe the use of cells from infiltrating ductal carcinoma of the breast, breast carcinoma, normal breast tissues, and infiltrating lobular carcinoma of the breast (page 17, third paragraph to page 18, first paragraph). Young et al. describe in claim 21 that the agent is an apoptosis-inducing agent. Young et al. describe a process of screening novel drugs using genes, including oncogenes (page 2, lines 12-17). Young et al. describe using a set of genes whose

Art Unit: 1631

expression, non-expression, or change (increase or decrease) in expression, are indicative of cancerous or non-cancerous status of a given cell (page 2, lines 22-25). Due to the open claim language of “a gene that corresponds to a polynucleotide” (claim 1) and “a polynucleotide comprising a nucleotide sequence corresponding to a gene” (claim 48), a prior art polynucleotide need not be 100% identical, although most of those described below are an exact match.

GenBank describes sequences (AP001082, AP000727, AA485973, and AA968812) which are 100% identical to SEQ ID NO: 110 of the instant invention. Young et al. describe sequences (ABL62840 and ABL63054) which are 100% identical to SEQ ID NO: 110 of the instant invention. GenBank describes sequences (AA478962) which are 100% identical to SEQ ID NO: 653 of the instant invention. Young et al. describe sequences (ABL63383, ABL64857, ABL65548, and ABL66020) which are 100% identical to SEQ ID NO: 653 of the instant invention. GenBank describes a sequence (N64489) which is 100% identical to SEQ ID NO: 683 of the instant invention. Young et al. describe sequences (ABL63413 and ABL63830) which are 100% identical to SEQ ID NO: 683 of the instant invention. GenBank describes a sequence (AA227221) which is 100% identical to SEQ ID NO: 767 of the instant invention. Young et al. describe sequences (ABL63497 and ABL63936) which are 100% identical to SEQ ID NO: 767 of the instant invention. GenBank describes a sequence (D80055) which is 99.8% identical to SEQ ID NO: 804 of the instant invention. Young et al. describe sequences (ABL61767 and ABL63534) which are 99.8% identical to SEQ ID NO: 804 of the instant invention. GenBank describes a sequence (N45300) which are 100% identical to SEQ ID NO: 820 of the instant invention. Young et al. describe a sequence (ABL63550) which is 100% identical to SEQ ID NO: 820 of the instant invention. GenBank describes sequences (D60118)

Art Unit: 1631

which are 97.9% identical to SEQ ID NO: 910 of the instant invention. Young et al. describe a sequence (ABL63640) which is 97.9% identical to SEQ ID NO: 910 of the instant invention. GenBank describes a sequence (H02533) which is 99.6% identical to SEQ ID NO: 1019 of the instant invention. Young et al. describe a sequence (ABL63749) which is 99.6% identical to SEQ ID NO: 1019 of the instant invention. GenBank describes sequences (AA010665) which are 100% identical to SEQ ID NO: 1040 of the instant invention. Young et al. describe sequences (ABL63770, ABL66331, and ABL67711) which are 100% identical to SEQ ID NO: 1040 of the instant invention. GenBank describes a sequence (N69022) which is 99.8% identical to SEQ ID NO: 1247 of the instant invention. Young et al. describe a sequence (ABL63977) which is 99.8% identical to SEQ ID NO: 1247 of the instant invention.

Kinzler et al. describe measuring a gene product that is elevated over that which is normally produced by non-cancerous cells (col. 5, lines 51-54). Kinzler et al. describe these elevated expressions may be present in various tumors such as from breast, lung, brain, bladder, prostate, liver, skin, colorectal, and stomach (col. 5, lines 55-60). Kinzler et al. describe using non-cancerous cells for determining baseline expression levels (col. 5, lines 60-67). Kinzler et al. describe methods and kits for detecting elevated expression and identifying compounds which interfere with gene products (col. 3, lines 19-24).

Robinson et al. state their invention provides a means to generate and monitor gene expression profiles resulting from cellular and physiological changes that can then be characterized for individual genes or groups of genes (col. 1, lines 4-10). Robinson et al. state their invention may be used to screen drug compounds that affect biological samples (col. 16, lines 48-52). Robinson et al. state that human cancer is a result of genetic changes that result in

Art Unit: 1631

alterations in the profile of expressed genes (col. 1, lines 30-33). Robinson et al. note the importance of methods that can measure the expression levels of thousands of genes to monitor the progression of cancer (col. 1, lines 33-39). Robinson et al. state their invention may be used to compare normal and cancerous tissue as well as to differentiate between cancerous tissue that is metastatic and non-metastatic (col. 15, lines 61-67). Robinson et al. describe using tissues from various types of organs as seen in Table 1. Robinson et al. state that various modifications and variations can be made to their invention (col. 30, lines 13-18). Young et al. describe genes analyzed therein exhibit differential expression over control non-cancerous cells. A person of ordinary skill in the art would have been motivated to combine other sequences from various parts of the body to the screening process presented by Robinson et al. and to compare them with known non-cancerous controls as stated by Kinzler et al. and Young et al. to check for the presence of gene expression alterations involved in normal and cancerous tissue. Therefore, it would have been obvious to one having ordinary skill in the art at the time the invention was made to test compounds on the various sequences described in the paragraph above which come from various parts of the body as well as comparing genes with known differential expression between cancerous and non-cancerous cells, as one of ordinary skill in the art would have a reasonable expectation of success to identify which compounds are effective in controlling expression and where in the body this control takes place, as stated by Robinson (col. 16, lines 48-57 and col. 22, lines 1-9 and 59-62).

Thus, Robinson et al., in view of GenBank (various Accession numbers), Young et al., and, and Kinzler et al. motivate claims 1-17, 47, and 48.

Art Unit: 1631

Conclusion

No claim is allowed.

Papers related to this application may be submitted to Technical Center 1600 by facsimile transmission. Papers should be faxed to Technical Center 1600 via the PTO Fax Center located in Crystal Mall 1. The faxing of such papers must conform with the notices published in the Official Gazette, 1096 OG 30 (November 15, 1988), 1156 OG 61 (November 16, 1993), and 1157 OG 94 (December 28, 1993) (See 37 CFR §1.6(d)). The CM1 Fax Center number is either (703) 308-4242 or (703) 305-3014.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Carolyn Smith, whose telephone number is (703) 308-6043. The examiner can normally be reached Monday through Friday from 8 A.M. to 4:30 P.M.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Michael Woodward, can be reached on (703) 308-4028.

Any inquiry of a general nature or relating to the status of this application should be directed to Legal Instruments Examiner Tina Plunkett whose telephone number is (703) 305-3524 or to the Technical Center receptionist whose telephone number is (703) 308-0196.

July 16, 2003


ARDIN H. MARSCHEL
PRIMARY EXAMINER

Sequence Match Listing for 09/954531

f- SEQ ID NO: 116

RESULT 4
 APO01082
 LOCUS Homo sapiens chromosome 11 clone CMB9-77P23 map 11q12, WORKING
 DEFINITION DRAFT SEQUENCE, 32 unordered pieces.
 ACCESSION APO01082
 VERSION APO01082.3 GI:8117229
 KEYWORDS HTG, HTGS, PHASE1, HTGS, DRAFT.
 SOURCE Homo sapiens DNA, clone: CMB9-77P23.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 130642)
 AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
 Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
 TITLE Homo sapiens 130,642 genomic DNA of 11q12
 JOURNAL Published Only in Database (2000)
 REFERENCE 2 (bases 1 to 130642)
 AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
 Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (25-JAN-2000) Masahira Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
 Japan (E-mail: hattori@gsc.riken.go.jp, Tel: 81-42-778-9923,
 URL: http://hgp.gsc.riken.go.jp/, Fax: 81-42-778-9924)
 On May 30, 2000 this sequence version replaced gi:6997796.
 COMMENT
 ----- Genome Center
 Center: RIKEN Genomic Sciences Center (GSC)
 Center code: RIKEN
 Web site: http://hgp.gsc.riken.go.jp/
 Contact: hattori@gsc.riken.go.jp
 ----- Project Information
 Center project name: HumDraft11
 Center clone name: CMB9-77P23
 ----- Summary Statistics
 Sequencing vector: PCR products; 100% of reads
 Chemistry: Dye-terminator; ET-amersham; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 109722 bases at least Q40
 Consensus quality: 118358 bases at least Q30
 Consensus quality: 123353 bases at least Q20
 Insert size: 127542; sum-of-ctrls
 Quality coverage: 4.10x in Q20 bases; sum-of-ctrls

NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their

order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved

1	14868	contig of	14868	bp	in	length
14969	24185	contig of	9217	bp	in	length
24286	32497	contig of	8212	bp	in	length
32598	39406	contig of	6809	bp	in	length
39507	44898	contig of	5392	bp	in	length
44999	50122	contig of	5124	bp	in	length
50223	57989	contig of	7767	bp	in	length
57989	58089	gap of	100	bp		
58089	64088	contig of	5999	bp	in	length
64088	64188	gap of	100	bp		
64188	68556	contig of	4368	bp	in	length
68557	68656	gap of	100	bp		
68657	72253	contig of	3603	bp	in	length
72260	72358	gap of	100	bp		
72358	76692	contig of	4333	bp	in	length
76693	76792	gap of	100	bp		
76793	80690	contig of	3898	bp	in	length
80691	80790	gap of	100	bp		
80791	84253	contig of	3463	bp	in	length
84254	84353	gap of	100	bp		
14868	14968	gap of	100	bp		
14969	24185	contig of	9217	bp	in	length
24186	24285	gap of	100	bp		
24286	32497	contig of	8212	bp	in	length
32498	32597	gap of	100	bp		
32598	39406	contig of	6809	bp	in	length
39407	39506	gap of	100	bp		
39507	44898	contig of	5392	bp	in	length
44899	44998	gap of	100	bp		
44999	50122	contig of	5124	bp	in	length
50123	50222	gap of	100	bp		
50223	57989	contig of	7767	bp	in	length
57989	58089	gap of	100	bp		
58089	64088	contig of	5999	bp	in	length
64088	64188	gap of	100	bp		
64188	68556	contig of	4368	bp	in	length
68557	68656	gap of	100	bp		
68657	72253	contig of	3603	bp	in	length
72260	72358	gap of	100	bp		
72358	76692	contig of	4333	bp	in	length
76693	76792	gap of	100	bp		
76793	80690	contig of	3898	bp	in	length
80691	80790	gap of	100	bp		
80791	84253	contig of	3463	bp	in	length
84254	84353	gap of	100	bp		

Sequence updated (02-FEB-2000)

NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

[illegible]

Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN

Web site: <http://hnp.gsc.riken.go.jp/>
Contact: hatorilegsc.riken.go.jp

Project Information
Center project name: HumDraft11
Center clone name: RPI1-679G21

----- Summary Statistics -----

Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 133607 bases at least Q40
Consensus quality: 142217 bases at least Q30
Consensus quality: 146720 bases at least Q20
Insert size: 149494; sum-of-contigs
Quality coverage: 4.03x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 40 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

```
1 11871 contig of 11871 bp in length
11972 22347 contig of 10376 bp in length
22348 22447: gap of 100 bp
22448 33540: contig of 11093 bp in length
33541 33640: gap of 100 bp
33641 41577: contig of 7937 bp in length
41578 41677: gap of 100 bp
41678 45975: contig of 4298 bp in length
45976 46075: gap of 100 bp
46076 53127: contig of 7052 bp in length
53128 53227: gap of 100 bp
53228 60314: contig of 7087 bp in length
60315 60414: gap of 100 bp
60415 65544: contig of 5130 bp in length
65545 65644: gap of 100 bp
65645 71027: contig of 5383 bp in length
71028 71127: gap of 100 bp
71128 75422: contig of 4295 bp in length
75423 75522: gap of 100 bp
75523 79274: contig of 3752 bp in length
79275 79374: gap of 100 bp
79375 84398: contig of 5024 bp in length
84399 84498: gap of 100 bp
84499 88990: contig of 4492 bp in length
88991 89090: gap of 100 bp
89091 93436: contig of 4346 bp in length
93437 93536: gap of 100 bp
93537 96655: contig of 3119 bp in length
96656 96755: gap of 100 bp
96756 99175: contig of 2420 bp in length
99176 99275: gap of 100 bp
99276 102659: contig of 3384 bp in length
102660 102759: gap of 100 bp
102760 105824: contig of 3065 bp in length
105825 105924: gap of 100 bp
105925 109361: contig of 3437 bp in length
109362 109461: gap of 100 bp
109462 112303: contig of 2842 bp in length
112304 112403: gap of 100 bp
112404 115484: contig of 3081 bp in length
115485 115884: gap of 100 bp
115885 118972: contig of 3388 bp in length
118973 119072: gap of 100 bp
119073 121620: contig of 2548 bp in length
121621 121720: gap of 100 bp
121721 124322: contig of 2602 bp in length
124323 124422: gap of 100 bp
124423 127088: contig of 2666 bp in length
127089 127188: gap of 100 bp
127189 130306: contig of 3118 bp in length
130307 130406: gap of 100 bp
130407 131809: contig of 1403 bp in length
131810 131909: gap of 100 bp
131910 133740: contig of 1831 bp in length
133741 133840: gap of 100 bp
133841 136109: contig of 2269 bp in length
136110 136209: gap of 100 bp
136210 137539: contig of 1330 bp in length
137540 137639: gap of 100 bp
137640 139390: contig of 1751 bp in length
139391 139490: gap of 100 bp
139491 140939: contig of 1449 bp in length
140940 141039: gap of 100 bp
141040 142493: contig of 1454 bp in length
142494 142593: gap of 100 bp
142594 144234: contig of 1641 bp in length
144235 144334: gap of 100 bp
144335 145850: contig of 1516 bp in length
145851 145950: gap of 100 bp
145951 147405: contig of 1455 bp in length
147406 147505: gap of 100 bp
147506 149002: contig of 1497 bp in length
149003 149102: gap of 100 bp
149103 150523: contig of 1059 bp in length
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Sequence updated (26-May-2000).

* NOTE: This is a 'working draft' sequence. It currently consists of 40 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* 1 11871: contig of 11871 bp in length
* 11872 11971: gap of 100 bp

```
11972 22347: contig of 10376 bp in length
22348 22447: gap of 100 bp
22448 33540: contig of 11093 bp in length
33541 33640: gap of 100 bp
33641 41577: contig of 7937 bp in length
41578 41677: gap of 100 bp
41678 45975: contig of 4298 bp in length
45976 46075: gap of 100 bp
46076 53127: contig of 7052 bp in length
53128 53227: gap of 100 bp
53228 60314: contig of 7087 bp in length
60315 60414: gap of 100 bp
60415 65544: contig of 5130 bp in length
65545 65644: gap of 100 bp
65645 71027: contig of 5383 bp in length
71028 71127: gap of 100 bp
71128 75422: contig of 4295 bp in length
75423 75522: gap of 100 bp
75523 79274: contig of 3752 bp in length
79275 79374: gap of 100 bp
79375 84398: contig of 5024 bp in length
84399 84498: gap of 100 bp
84499 88990: contig of 4492 bp in length
88991 89090: gap of 100 bp
89091 93436: contig of 4346 bp in length
93437 93536: gap of 100 bp
93537 96655: contig of 3119 bp in length
96656 96755: gap of 100 bp
96756 99175: contig of 2420 bp in length
99176 99275: gap of 100 bp
99276 102659: contig of 3384 bp in length
102660 102759: gap of 100 bp
102760 105824: contig of 3065 bp in length
105825 105924: gap of 100 bp
105925 109361: contig of 3437 bp in length
109362 109461: gap of 100 bp
109462 112303: contig of 2842 bp in length
112304 112403: gap of 100 bp
112404 115484: contig of 3081 bp in length
115485 115884: gap of 100 bp
115885 118972: contig of 3388 bp in length
118973 119072: gap of 100 bp
119073 121620: contig of 2548 bp in length
121621 121720: gap of 100 bp
121721 124322: contig of 2602 bp in length
124323 124422: gap of 100 bp
124423 127088: contig of 2666 bp in length
127089 127188: gap of 100 bp
127189 130306: contig of 3118 bp in length
130307 130406: gap of 100 bp
130407 131809: contig of 1403 bp in length
131810 131909: gap of 100 bp
131910 133740: contig of 1831 bp in length
133741 133840: gap of 100 bp
133841 136109: contig of 2269 bp in length
136110 136209: gap of 100 bp
136210 137539: contig of 1330 bp in length
137540 137639: gap of 100 bp
137640 139390: contig of 1751 bp in length
139391 139490: gap of 100 bp
139491 140939: contig of 1449 bp in length
140940 141039: gap of 100 bp
141040 142493: contig of 1454 bp in length
142494 142593: gap of 100 bp
142594 144234: contig of 1641 bp in length
144235 144334: gap of 100 bp
144335 145850: contig of 1516 bp in length
145851 145950: gap of 100 bp
145951 147405: contig of 1455 bp in length
147406 147505: gap of 100 bp
147506 149002: contig of 1497 bp in length
149003 149102: gap of 100 bp
149103 150523: contig of 1059 bp in length
```

Mon Jun 30 08:42:14 2003

us-09-954-

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* 150524 150623: gap of 100 bp
* 150624 152235: contig of 1612 bp in length
* 152236 152335: gap of 100 bp
* 152336 153394: contig of 1059 bp in length.
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                    /db_xref="taxon:9606"
                    /chromosome="11"
                    /map="11q12"
                    /clone="RP11-679G21"
 misc_feature        1..11871
                    /note="assembly_fragment"
 misc_feature        11972..22347
                    /note="assembly_fragment"
 misc_feature        22448..33540
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 misc_feature        33641..41577
                    /note="assembly_fragment"
 misc_feature        41678..45975
                    /note="assembly_fragment clone_end:T7 vector_side:left"
 misc_feature        46076..53127
                    /note="assembly_fragment"
 misc_feature        53228..60314
                    /note="assembly_fragment"
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Query Match          100.0%; Score 382; DB 2; Length 153394;
Best Local Similarity 100.0%; Pred. No. 7.9e-75;
Matches 382; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY      1 AATTCCTTTTGTAGCTCATTGGCTATCCTTAGCGTACATTATGTATGGCCCAACACAATTC 60
         |||
Db       71881 AATTCCTTTTGTAGCTCATTGGCTATCCTTAGCGTACATTATGTATGGCCCAACACAATTC 71940

QY      61 TTCTTCCACTGTAGCCAGGGAAGCCAAAAGATTGGACACTCTTGTTTAAATAGACTAT 120
         |||
Db       71941 TTCTTCCACTGTAGCCAGGGAAGCCAAAAGATTGGACACTCTTGTTTAAATAGACTAT 72000

QY      121 CTTTTTACCCTTTTATTTGTTCCAACCTCAGGATAAATATCCAAGTATCTAGAGGGTCTAT 180
         |||
Db       72001 CTTTTTACCCTTTTATTTGTTCCAACCTCAGGATAAATATCCAAGTATCTAGAGGGTCTAT 72060

QY      181 GTGTGCTATCTATACAATAAAAGATAGTTATATAAAAATGAAGAGTTCTCCATACCATTA 240
         |||
Db       72061 GTGTGCTATCTATACAATAAAAGATAGTTATATAAAAATGAAGAGTTCTCCATACCATTA 72120

QY      241 TATAAACAGGAGGTTTTACAGGCATTAGTGATACTCTGTTGGACTCAATGGGTTTTTTTC 300
         |||
Db       72121 TATAAACAGGAGGTTTTACAGGCATTAGTGATACTCTGTTGGACTCAATGGGTTTTTTTC 72180

QY      301 TCTCTTATAGCTATGAAAGACTTTATGCCAGTCCAAAATATACAATGTTGAAAGACAGGT 360
         |||
Db       72181 TCTCTTATAGCTATGAAAGACTTTATGCCAGTCCAAAATATACAATGTTGAAAGACAGGT 72240

QY      361 TTTGAAATAAATATTCTCCCA 382
         |||
Db       72241 TTTGAAATAAATATTCTCCCA 72262
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ALIGNMENTS

Gr SEQ ID NO: 110

RESULT 1
AA485973
LOCUS AA485973 382 bp mRNA linear EST 05-MAR-1998
DEFINITION ab11e10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone
IMAGE:840522 3' similar to contains MER30.t3 MER30 repetitive
element ;, mRNA sequence.
ACCESSION AA485973
VERSION AA485973.1 GI:2215124
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 382)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE WashU-NCI human EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 967 Std Error: 0.00

ALIGNMENTS

RESULT 1

ABL62840

ID ABL62840 standard; DNA; 382 BP.

XX

AC ABL62840;

XX

DT 15-MAY-2002 (first entry)

XX

DE Breast cancer related gene sequence SEQ ID NO:1177..

XX

KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;

KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;

KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;

KW gene; ds.

XX

OS Homo sapiens.

XX

PN WO200194629-A2.

XX

PD 13-DEC-2001.

XX

PF 30-MAY-2001; 2001WO-US10838.

XX

PR 05-JUN-2000; 2000US-209473P.

PR 05-JUN-2000; 2000US-209531P.

PR 18-SEP-2000; 2000US-233133P.

PR 18-SEP-2000; 2000US-233617P.

PR 20-SEP-2000; 2000US-234009P.

PR 20-SEP-2000; 2000US-234034P.

PR 20-SEP-2000; 2000US-234052P.

PR 22-SEP-2000; 2000US-234509P.

PR 22-SEP-2000; 2000US-234567P.

for SEQ ID NO: 110

1 AATCTTTTTCAGCTCATTTGGCTATCCCTAGGTCATATGATGGCCCAACACATTC 60

28-SEP-2000; 2000US-236028P.
28-SEP-2000; 2000US-236032P

KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
 KW gene; ds.

OS Homo sapiens.

PN WO200194629-A2.

PD 13-DEC-2001.

PF 30-MAY-2001; 2001WO-US10838.

XX 05-JUN-2000; 2000US-209473P.
 PR 05-JUN-2000; 2000US-209531P.
 PR 18-SEP-2000; 2000US-233133P.
 PR 18-SEP-2000; 2000US-233617P.
 PR 20-SEP-2000; 2000US-234009P.
 PR 20-SEP-2000; 2000US-234034P.
 PR 20-SEP-2000; 2000US-234052P.
 PR 22-SEP-2000; 2000US-234509P.
 PR 22-SEP-2000; 2000US-234567P.
 PR 25-SEP-2000; 2000US-234923P.
 PR 25-SEP-2000; 2000US-234924P.
 PR 25-SEP-2000; 2000US-235077P.
 PR 25-SEP-2000; 2000US-235082P.
 PR 25-SEP-2000; 2000US-235134P.
 PR 25-SEP-2000; 2000US-235280P.
 PR 26-SEP-2000; 2000US-235637P.
 PR 26-SEP-2000; 2000US-235638P.
 PR 27-SEP-2000; 2000US-235711P.
 PR 27-SEP-2000; 2000US-235720P.
 PR 27-SEP-2000; 2000US-235840P.
 PR 28-SEP-2000; 2000US-236028P.
 PR 28-SEP-2000; 2000US-236032P.
 PR 28-SEP-2000; 2000US-236033P.
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 PR 28-SEP-2000; 2000US-236109P.
 PR 28-SEP-2000; 2000US-236111P.
 PR 29-SEP-2000; 2000US-236842P.
 PR 29-SEP-2000; 2000US-236891P.
 PR 02-OCT-2000; 2000US-237172P.
 PR 02-OCT-2000; 2000US-237173P.
 PR 02-OCT-2000; 2000US-237278P.
 PR 02-OCT-2000; 2000US-237294P.
 PR 02-OCT-2000; 2000US-237295P.
 PR 02-OCT-2000; 2000US-237315P.
 PR 03-OCT-2000; 2000US-237425P.
 PR 03-OCT-2000; 2000US-237598P.
 PR 03-OCT-2000; 2000US-237604P.
 PR 03-OCT-2000; 2000US-237606P.
 PR 03-OCT-2000; 2000US-237608P.
 PR 01-NOV-2000; 2000US-244867P.
 PR 01-NOV-2000; 2000US-245084P.

XX (AVAL-) AVALON PHARM.

PI Young PE, Augustus M, Carter KC, Edner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;

XX WPI; 2002-188264/24.

XX Screening for anti-neoplastic agent involves exposing cells to a
 PT chemical agent to be tested for anti-neoplastic activity, and
 PT determining a change in expression of a gene of a signature gene set
 XX Claim 1; SEQ ID 1720; 44pp; English.

XX The present invention describes a method (M1) for screening for an
 CC anti-neoplastic agent. The method involves exposing cells to a chemical
 CC agent to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)

RESULT 2
 ABL63383
 ID ABL63383 standard; DNA, 378 BP.
 XX
 AC ABL63383;
 XX
 DT 15-MAY-2002 (first entry)
 XX
 Breast cancer related gene sequence SEQ ID NO:1720.

for SEA ID NO:653

CGTCTGGGATACCAAGTTTCATGCAGCAGCAAATAAACAATATATAATCATCAATGC 120

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL1664) to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, nasopharyngeal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms' tumour.

[illegible]

PR 29-SEP-2000; 2000US-236891P.

Qy	1	TTTTTTTTTTTTTTTTTGGTCATCTACATTTCACTTTATTTATTTAACTTTATCATTA	60
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Qy	121	ACTTTGATATTTTAAACATACATAAAATATGAGTAATGAGAGCTATGTTACATGATA	180
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Db	181	TTTTTACAAAGAAAAAGATGACCTTTATATATACATGACATGAAATTTATCATTTA	240
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Db	241	AATTTTGGATTCATATGATGTAAATATGATATATCAAAACAATTTACTATTTATAGA	300
Qy	301	ACCAATTTGATATTTTGTCATTTAAATATATGATATCTATGTAATGAGTACTTATATAA	360
Db	301	ACCAATTTGATATTTTGTCATTTAAATATATGATATCTATGTAATGAGTACTTATATAA	360

Mon Jun 30 08:42:15 2003

us-09-954-5

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Db      301 ACCAATTGATATTTTGTCAATTTAAAAATAATGAATACTATGTAAATGAGTACTTATAAAA 360
Qy      361 ATATTTT TAGGCAAAAAG 378
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Db      361 ATATTTT TAGGCAAAAAG 378
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for SEA ID NO: 653

us-09-954

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FEATURES
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/db_xref="GDB:597686"
/db_xref="taxon:9606"
/clone="IMAGE:753993"
/clone_1lb="Scars NBHNPu_51"
/tissue-type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pTY73D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NBH, pregnant uterus
NBHPU, and fetal heart NBH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
BASE COUNT
150 a
41 c 40 g 147 t
ORIGIN

```

N64489 YZ99067 .438 bp mRNA linear EST 01-MAR-1999
 Clone IMAGE:290340 3', mRNA sequence.
 N64489
 EST.
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 438)
 Biller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
 M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
 Rifkin, L., Rohlfing, T., Soares, M., Tao, F., Trevisakis, E., Waterston
 R., Williamson, A., Wohlmann, P. and Wilson, R..
 The WashU-Merck EST Project
 Unpublished (1995)
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LNC; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: m3 -40 forward
 High quality sequence stop: 416.

Location/Qualifiers
1. .438

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Db	121	GAGAGTAATTAATACAAAGATGATGTGTGTTTCTGATTTCAATATGTTATCATAGTT	180
OY	181	GTCAACTTTTCATCTCAAAAAAACCCCTATTTTATACCTAATTTTAAATTAATAATTTT	240
Db	181	GTCAACTTTTCATCTCAAAAAAACCCCTATTTTATACCTAATTTTAAATTAATAATTTT	240
OY	241	TCAGTTTGTATTAAAGAGACTCCCCAAATTATATGATTTCCAACTTCATTAATAACCTTA	300
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ALIGNMENTS

Seq ID NO: 683

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DT 15-MAY-2002 (first entry)
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KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US10838.
XX
PR 05-JUN-2000; 2000US-209473P.
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PR 18-SEP-2000; 2000US-233133P.
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PR 22-SEP-2000; 2000US-234567P.

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 PR 26-SEP-2000; 2000US-235637P.
 PR 26-SEP-2000; 2000US-235638P.
 PR 27-SEP-2000; 2000US-235711P.
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 PR 01-NOV-2000; 2000US-244867P.
 PR 01-NOV-2000; 2000US-245084P.

(AVAL-) AVALON PHARM.

XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;

XX WPI: 2002-188264/24.

PT Screening for anti-neoplastic agent involves exposing cells to a
 PT chemical agent to be tested for anti-neoplastic activity, and
 PT determining a change in expression of a gene of a signature gene set

PS Claim 1; SEQ ID 1750; 44p; English.

XX The present invention describes a method (M1) for screening for an
 CC anti-neoplastic agent. The method involves exposing cells to a chemical
 CC agent to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
 CC activity and can be used in gene therapy. M1 can be used for screening
 CC an anti-neoplastic agent, and can be used for producing a product which
 CC is the data collected with respect to the anti-neoplastic agent as a
 CC result of M1, and the data is sufficient to convey the chemical
 CC structure and/or properties of the agent. M1 can be used in the
 CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
 CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
 CC carcinoma, papillary carcinoma and Wilms' tumour.

XX Sequence 438 BP; 155 A; 74 C; 69 G; 140 T; 0 other;

Query Match 100.0%; Score 438; DB 24; Length 438;
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 Db 361 TTGGAACCTGCTGTGCTGAGACCAAGTTCACTTGCGCTCTCCATGGGTACTTAC 420
 OY 421 TGGCCCAAGCCAAAGCTG 438
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 AC ABL63830;
 XX
 DF 15-MAY-2002 (first entry)
 XX
 DE Breast cancer related gene sequence SEQ ID NO:2167.
 XX
 KW Human: cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cytostatic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;
 KW gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200194629-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 30-MAY-2001; 2001WO-US10838.
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PR	01-NOV-2000	2000US-2445084.P

us-09-954-5

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Mon Jun 30 08:42:16 2003

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Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTCGAAATTAAGAGATGTAATTTATTTGGTAATAATAGATATAAAATTAACACCTATTTTAAATATAT 60

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ALIGNMENTS

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for SEQ ID NO: 767

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AC ABL63497;
XX
DT 15-MAY-2002. (first entry)
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DE Breast cancer related gene sequence SEQ ID NO:1834.
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KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
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PF 30-MAY-2001; 2001WO-US10838.
XX
PR 05-JUN-2000; 2000US-209473P.
PR 05-JUN-2000; 2000US-209531P.
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PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234509P.
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PR		
(AVAL-)	AVALON PHARM.	
PR		

XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppe DR, Weaver Z;
XX
XX
DR WPL; 2002-188264/24.
XX
XX
PT Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set
XX
XX Claim 1; SEQ ID 1834; 44pp; English.

CC The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I1) of a signature gene set, where (I1)
CC comprises a sequence (S) selected from 8447 sequences (given in AB161564
CC to AB170110), or is at least 93% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I1) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilms's tumour.

SQ Sequence 381 BP; 135 A; 72 C; 53 G; 121 T; 0 other;

Query Match	100.0%	Score 381;	DB 24;	Length 381;
Best Local Similarity	100.0%	Pred. NO.	1.5e-75;	
Matches 381;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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QY	181	ATATCAGTGCTTCAGAGTTTTCACAAACAGTTTCACAAAGATTAAGTCCCAATCAG	240
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AC ABL63936;

DT 15-MAY-2002 (first entry)

DE Breast cancer related gene sequence SEQ ID NO:2273.

KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;

KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;

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HONG KONG

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XX 13-DEC-2001
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XX 30-MAY-2001. 2001EO-PC10839
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PR 25-SEP-2000; 2000TS-234923P
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Mon Jun 30 08:42:17 2003

us-09-954-

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ACCESSION D80055
VERSION D80055.1 GI:1177932
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Primates; Catarrhini; Homiidae; Homo.
AUTHORS 1 (bases 1 to 517)
Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M.,
Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shiomiyu, H., Takachi,
'A.', Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y., Maekawa, H.,
Shin, S. and Nakamura, Y.
COMMENT Unpublished (1995)
Contact: Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co., Ltd
463-10 Kagasudo Kawachi-cho, Tokushima, Tokushima, 771-01 Japan
Tel: 0886-65-2888
Fax: 0886-37-1035.
FEATURES
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Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ALIGNMENTS

for SEQ ID NO: 807

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DT 15-MAY-2002 (first entry)
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KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
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PD 13-DEC-2001.
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PF 30-MAY-2001; 2001WO-US10838.
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PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234509P.
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PR	25-SEP-2000	2000US-234923P
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PR	28-SEP-2000	2000US-236032P
PR	28-SEP-2000	2000US-236033P
PR	28-SEP-2000	2000US-236034P
PR	28-SEP-2000	2000US-236109P
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PR	29-SEP-2000	2000US-236891P
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PR	02-OCT-2000	2000US-237173P
PR	02-OCT-2000	2000US-237278P
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PR	02-OCT-2000	2000US-237295P
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PR	01-NOV-2000	2000US-245084P

PA	(AVAL-) AVALON PHARM.
XX	
PI	Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S,
PI	Soppet DR, Weaver Z;
XX	
WPI	2002-188264/24.
DR	
XX	

Claim 1; SEQ ID 104; 44pp; English.

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in AB161564 to AB170110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms' tumour.

Sequence 517 BP; 188 A; 119 C; 91 G; 117 T; 2 other;

Query Match	99.88;	Score 515.8;	DB 24;	Length 517;
Best Local Similarity	100.08;	Pred. No. 4e-132;		
Matches 517; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

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QY	121	CCATTTCCCATCCCTGCGACATTAATTAATTAATAACCCAAAGACACACCTTAACAAGAAA	180
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QY	181	AACACACGTACGTATGAAAAAAGCAATGTCCATCTGCTCAGTCCAAATACCTTAT	240
Db	181	AACACACGTACGTATGAAAAAAGCAAAATGTCCATCTGCTCAGTCCAAATACCTTAT	240
QY	241	GAATGTCTTCCCCCAGCTAAACCCCTACCCCATGGAATGATTAAGAAATGTAGACAA	300
Db	241	GAATGTCTTCCCCCAGCTAAACCCCTACCCCATGGAATGATTAAGAAATGTAGACAA	300
QY	301	CCCTTAGGGGAGACTTGGAACTCTGCTTATACGACAAAGCTCAGTGAAGATAGTAGA	360
Db	301	CCCTTAGGGGAGACTTGGAACTCTGCTTATACGACAAAGCTCAGTGAAGATAGTAGA	360
QY	361	GTAGGAATCTGTTTGGCAGTGAACACCTGATTAACCTTCTTTTCAAAATTTGGATGAT	420
Db	361	GTAGGAATCTGTTTGGCAGTGAACACCTGATTAACCTTCTTTTCAAAATTTGGATGAT	420
QY	421	TGCAGAGAAACAGGTAGAGTTTGAAGGTCACAGACTCTTAACAGAGACTGATCCCTGTTCC	480
Db	421	TGCAGAGAAACAGGTAGAGTTTGAAGGTCACAGACTCTTAACAGAGACTGATCCCTGTTCC	480
QY	481	TCAACCGTAAACAGGTGGGBAGACTGCCAAATCCTGGGT	517
Db	481	TCAACCGTAAACAGGTGGGBAGCTGCCAAATCCTGGGT	517

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ID	ABL63534 standard; DNA; 517 BP.
YV	

AC ABL63534 ;

DT 15-MAY-2002 (first entry)
YY

Breast cancer related gene sequence SEQ ID NO:1871.

Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
gene; ds.

OS Homo sapiens.

PN : WO200194629-A2.
XY :

PD 13-DEC-2001.
YY

PE 30-MAY-2001; 2001WO-US10838.
XX

PR	05-JUN-2000; 2000DS-209473P
PR	05-JUN-2000; 2000DS-209531P

PR 18-SEP-2000: 2000TS-233617P

PR	20-SEP-2000: 2000US-23403AP
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PR 22-SEP-2000; 2000US-234509P.

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PR 25-SEP-2000; 2000US-235134P.

PR 26-SEP-2000; 2000US-235637P.
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 PR 02-OCT-2000; 2000US-237172P.
 PR 02-OCT-2000; 2000US-237173P.
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 PR 02-OCT-2000; 2000US-237294P.
 PR 02-OCT-2000; 2000US-237295P.
 PR 02-OCT-2000; 2000US-237316P.
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 PR 01-NOV-2000; 2000US-244667P.
 PR 01-NOV-2000; 2000US-245084P.
 PA (AVAIL-) ANALON PERAM.
 XX
 XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;
 XX
 XX WPI; 2002-188264/24.
 DR
 XX
 XX
 PT Screening for anti-neoplastic agent involves exposing cells to a
 PT chemical agent to be tested for anti-neoplastic activity, and
 PT determining a change in expression of a gene of a signature gene set -
 XX
 PS Claim 1; SEQ ID 1871; 44pp; English.

CC The present invention describes a method (M1) for screening for an
 CC anti-neoplastic agent. The method involves exposing cells to a chemical
 CC agent to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL6164
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
 CC activity and can be used in gene therapy. M1 can be used for screening
 CC an anti-neoplastic agent, and can be used for producing a product which
 CC is the data collected with respect to the anti-neoplastic agent as a
 CC result of M1, and the data is sufficient to convey the chemical
 CC structure and/or properties of the agent. M1 can be used in the
 CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
 CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
 CC carcinoma, papillary carcinoma and Wilms' tumour.
 XX
 SQ Sequence 517 BP; 188 A; 119 C; 91 G; 117 T; 2 other;

Query Match 99.8%; Score 515.8; DB 24; Length 517;
 Best Local Similarity 100.0%; Pred. No. 4e-132;
 Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 CCAATTTCAAAAAGTTTATTTGAAAGATGAGAGAAATTAACAGAGAGTTCAT 60
 |||
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OY 121 CCAATTTCCCAATCCCTGGCACAAATTAATTAACACCAACCAAGCACACTACAGAGAA 180
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 DB 121 CCAATTTCCCAATCCCTGGCACAAATTAATTAACACCAACCAAGCACACTACAGAGAA 180
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 OY 181 AACAGAGTACGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
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 DB 181 AACAGAGTACGTATGATGATGATGATGATGATGATGATGATGATGATGAT 240
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 DB 241 GAAATGTCCTCCCGAGCTTAACCTTACCACCTGATGATGATGATGATGATGAT 300
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 OY 361 GTAGTGAATCTGTTGGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 420
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 DB 361 GTAGTGAATCTGTTGGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 420
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 DB 421 TGCAGAGAACAGTAGAGTGTGAGGCTCACAGACTTCTTAACAGAGTGAATCCGTTGCC 480
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 OY 481 TCAACCGTAAACAGTGGGGGAGCTGCCAAATCCTGGGT 517
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US-09-954-

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/tissue_type="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pUT73D (Pharmacia) with a modified
polylinker V.Type: phagemid; Site_1: Not I; Site_2: Eco RI
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1st strand cDNA was primed with a Not I - oligo(dT)
primer 15'
TGTTACCAATCTGAAGTGAGCGGCCGCATTATTTTTTTTTTTTTTTT 3'
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pUT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis
lesions from one patient was kindly provided by Dr. Kevin
G. Becker (NINDS/NIH).
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ALIGNMENTS

for SEQ ID NO: 820

RESULT 1
ABL63550
ID ABL63550 standard; DNA; 595 BP.
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AC ABL63550;
XX
DT 15-MAY-2002 (first entry)
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DE Breast cancer related gene sequence SEQ ID NO:1887.
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KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US10838.
XX
PR 05-JUN-2000; 2000US-209473P.
PR 05-JUN-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234509P.
PR 22-SEP-2000; 2000US-234567P.

PR 25-SEP-2000; 2000US-234933P
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PR 03-OCT-2000; 2000US-237598P
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PR 03-OCT-2000; 2000US-237606P
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PR 01-NOV-2000; 2000US-244867P
PR 01-NOV-2000; 2000US-245084P
XX XX

(AVAIL-) AVALON PEARL.

Young PE, Augustus M, Carter KC, Edner R, Endress G, Horrigan S;
Soppet DR, Weaver Z;
WPI; 2002-188264/24.
Screening for anti-neoplastic agent involves exposing cells to a
chemical agent to be tested for anti-neoplastic activity, and
determining a change in expression of a gene of a signature gene set
Claim 1; SEQ ID 1887; 44pp; English.

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set comprising a sequence (S) selected from 8447 sequences (given in AB61664 to AB610110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms' tumour.

SQ Sequence 595 BP; 193 A; 114 C; 99 G; 186 T; 3 other;

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Best Local Similarity	100.0%	Pred	NO			2	50-136

Matches	595;	Conservative	0;	Mismatches	0;	Indels	0;
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Db 1 GACAAAAAATATCTGTTTATTTATTTATTTAGATTCAGATTTCAATTCAGTACTGACACCAAGCATCA 60

OY 61 CAACGTGGCGTTGGCGTTATTTATTAACAATCCAAACGTGTTCCATCAGAGAAGCGTAAAGCTCA 120

Db 61 CAACGTGGCGTTGGCGTTATTTATTAACAATCCAAACGTGTTCCATCAGAGAAGCGTAAAGCTCA 120

OY 121 GGTGCGAATGATTGTTATTAATTAATTAAGTCCCTGGTTTCCTGATAGAAAAAGGCTATCA 180

Db 121 GGTGCGAATGATTGTTATTAATTAATTAAGTCCCTGGTTTCCTGATAGAAAAAGGCTATCA 180

OY 181 ACAAGCATTTGTTTATTCACACAACAAAAGTATTAATTAAGTATATCCACTAGTAAATCTT 240

Db 181 ACAAGCATTTGTTTATTCACACAACAAAAGTATTAATTAAGTATATCCACTAGTAAATCTT 240

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Db 301 TTCAATTTTCCAGTCCCTTTTGGCAAAAATTTATTTACAAATGTCATATAATGCTCCAA 360

OY 361 GGTGGGCAATGAAAAAAATATACACATGACCGATGCTTGGTCAGAAAATTAAGTCAACAT 420

Db 361 GGTGGGCAATGAAAAAAATATACACATGACCGATGCTTGGTCAGAAAATTAAGTCAACAT 420

OY 421 ATTAAAAATTAATCTTCAGCTGTATGTTTATAGAGTGCCTTAAACAGAAAGTATGTATPAA 480

Db 421 ATTAAAAATTAATCTTCAGCTGTATGTTTATAGAGTGCCTTAAACAGAAAGTATGTATPAA 480

OY 481 GGTGGGTGTTGTGGCATGGGGGACAATGATATGCTGATGTGACAAATTAAGGCTCTTAA 540

Db 481 GGTGGGTGTTGTGGCATGGGGGACAATGATATGCTGATGTGACAAATTAAGGCTCTTAA 540

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Db 541 ACAACAGGATCTTGGGTTTCCATGCGCTCTTCTACCAAGTCTCTTAAACCCCTGC 595

for SET ID NO: 910

Mon Jun 30 08:42:18 2003

us-09-95.

RESULT 1
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LOCUS
DEFINITION
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sapiens CDNA clone GEN-087A05 3', mRNA sequence.
VERSION
D60118
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
REFERENCE
AUTHORS
Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
1 (bases 1 to 389)
Fujitani, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M.,
Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shimomura, H., Takachi,
A., Takeda, S., Matanabe, T., Takahashi, E., Hirai, Y., Maekawa, H.,
Shin, S. and Nakamura, Y.
Fujitani et al. (1995)
TITLE
JOURNAL
COMMENT
Unpublished (1995)
Contact: Tsutomu Fujiwara
Otsuka GEN Research Institute
463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
Tel: 0886-65-2888
Fax: 0886-37-1035.
FEATURES
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Best Local Similarity 100.0%; Pred. No. 1.2e-95;
Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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ALIGNMENTS

RESULT 1

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ID ABL63640 standard; DNA; 389 BP.

XX

AC ABL63640;

XX

DT 15-MAY-2002 (first entry)

XX

DE Breast cancer related gene sequence SEQ ID NO:1977.

XX

KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;

KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;

KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;

KW gene; ds.

XX

OS Homo sapiens.

XX

PN WO200194629-A2.

XX

PD 13-DEC-2001.

XX

PF 30-MAY-2001; 2001WO-US10838.

XX

PR 05-JUN-2000; 2000US-209473P.

PR 05-JUN-2000; 2000US-209531P.

PR 18-SEP-2000; 2000US-233133P.

PR 18-SEP-2000; 2000US-233617P.

PR 20-SEP-2000; 2000US-234009P.

PR 20-SEP-2000; 2000US-234034P.

PR 20-SEP-2000; 2000US-234052P.

PR 22-SEP-2000; 2000US-234509P.

PR 22-SEP-2000; 2000US-234567P.

for SEQ ID NO: 910

PR 25-SEP-2000; 2000US-234923P.
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 PR 01-NOV-2000; 2000US-244867P.
 PR 01-NOV-2000; 2000US-245084P.

(AVAL-) AVALON PHARM.

Young PE, Augustus M, Carter KC, Edner R, Endress G, Horrigan S;
 Sopet DR, Weaver Z;
 WPI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a
 chemical agent to be tested for anti-neoplastic activity, and
 determining a change in expression of a gene of a signature gene set

Claim 1; SEQ ID 1977; 4app; English.

PS The present invention describes a method (M1) for screening for an
 XX anti-neoplastic agent. The method involves exposing cells to a chemical
 CC agent to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in ABU61664
 CC to ABU70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
 CC activity and can be used in gene therapy. M1 can be used for screening
 CC an anti-neoplastic agent, and can be used for producing a product which
 CC is the data collected with respect to the anti-neoplastic agent as a
 CC result of M1, and the data is sufficient to convey the chemical
 CC structure and/or properties of the agent. M1 can be used in the
 CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
 CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
 CC carcinoma, papillary carcinoma and Wilms' tumour.

XX Sequence 389 BP; 132 A; 65 C; 87 G; 92 T; 13 other;

Query Match 97.9%; Score 380.8; DB 24; Length 389;
 Best Local Similarity 100.0%; Pred. No. 1.7e-38;
 Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	1	AAACTGAGGGAACCTATGCTTTAATAGACACTGAAATCACAAGRGGAAGCCCAAGT	60
Qy	61	GCCTAGCATCTCATTAATAAATATGAVGTTCTTTTACATGTAATTTCAATATATA	120
Db	61	GCCTAGCATCTCATTAATAAATATGAVGTTCTTTTACATGTAATTTCAATATATA	120
Qy	121	MANGTTAATGTCGVAATGTCGTAATTTACAAAAGTCCACGTAAGCCCAAGATGG	180
Db	121	MANGTTAATGTCGVAATGTCGTAATTTACAAAAGTCCACGTAAGCCCAAGATGG	180
Qy	181	CTAANNCTGATTAAGGVAAGTGAATSCAGTGAAGAGTGTCTGAGAGGGCAGAGGC	240
Db	181	CTAANNCTGATTAAGGVAAGTGAATSCAGTGAAGAGTGTCTGAGAGGGCAGAGGC	240
Qy	241	CACAGTGTCTCTGACAGGAACATCTTTGAAGATCTGNAACAACAAGGCCAGTTCA	300
Db	241	CACAGTGTCTCTGACAGGAACATCTTTGAAGATCTGNAACAACAAGGCCAGTTCA	300
Qy	301	CAACACAGGTACACATCTTTTGAATAGGACACAGCAATAGTGATGAATTTATACGT	360
Db	301	CAACACAGGTACACATCTTTTGAATAGGACACAGCAATAGTGATGAATTTATACGT	360
Qy	361	TTGACCTGTGCTTACTTACTGAAGCA	389
Db	361	TTGACCTGTGCTTACTTACTGAAGCA	389

1 AAACGTAGGGAACCTATGCTTTAATAGACACTGAAATCACAAGRGGAAGCCCAAGT 60
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16-60-87

```

FEATURES
Source
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 739 Std Error: 0.00
Seq primer: M13RPI
High quality sequence stop: 331.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="GDB:563320"
/db_xref="taxon:9606"
/clone="IMAGE:151245"
/clone_lib="Scares Placenta Nb2Hp"
/sex="Female"
/dev_stage="placenta obtained at birth (full term)"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: placenta; Vector: pT773D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
AATCGAGAGAAATTCGCGCGCAGAGAAATTTTTTTTTTTTTTTT 3'],
(double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT773 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT
130 a 78 c 70 g 165 t 2 others
ORIGIN

```

ALIGNMENTS

for SEQ ID NO:1019

RESULT 1
ABL63749
ID ABL63749 standard; DNA; 445 BP.
XX
AC ABL63749;
XX
DT 15-MAY-2002 (first entry)
XX
DE Breast cancer related gene sequence SEQ ID NO:2086.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US10838.
XX
PR 05-JUN-2000; 2000US-209473P.
PR 05-JUN-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234509P.
PR 22-SEP-2000; 2000US-234567P.

Young PE, Augustus M, Carter KC, Edner R, Endress G, Horrigan S,
Soppet DR, Weaver Z;
WPI; 2002-188264/24.

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in AB161664 to AB170110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms' tumour.

Query Match	Score	DB	Length
Best Local Similarity	99.68;	443;	445;
Matches 445.	100.08;	Pred. No. 1e-89;	

Local Similarity 100.08; Pred. No. 1e-89; Length 445;
Matches 445; Conservative 0; Mismatches 0

0;	Indels	0;	Gaps	0;
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[illegible]

```

FEATURES
SOURCE
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="GDB:1276003"
/db_xref="taxon:9606"
/clone="IMAGE:359459"
/clone_lib="Soares_fetal_heart_NBHH19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ; heart; Vector: pT73D (Pharmacia) with a modified polylinker; Site_1: Not I ; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTCGAGCGGCCGCATCTTTTTTTTTTTTTTTT 3'] , double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Patino Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBHH19W."

```

ALIGNMENTS

RESULT 1
ABL63770

ID ABL63770 standard; DNA; 403 BP.

XX

AC ABL63770;

XX

DT 15-MAY-2002 (first entry)

XX

DE Breast cancer related gene sequence SEQ ID NO:2107.

XX

KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;

KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;

KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;

KW gene; ds.

XX

OS Homo sapiens.

XX

PN WO200194629-A2.

XX

PD 13-DEC-2001.

XX

PF 30-MAY-2001; 2001WO-US10838.

XX

PR 05-JUN-2000; 2000US-209473P.

PR 05-JUN-2000; 2000US-209531P.

PR 18-SEP-2000; 2000US-233133P.

PR 18-SEP-2000; 2000US-233617P.

PR 20-SEP-2000; 2000US-234009P.

PR 20-SEP-2000; 2000US-234034P.

PR 20-SEP-2000; 2000US-234052P.

PR 22-SEP-2000; 2000US-234509P.

PR 22-SEP-2000; 2000US-234567P.

for SEQ ID NO:1040

PR	25-SEP-2000	2000US-234923P
PR	25-SEP-2000	2000US-234924P
PR	25-SEP-2000	2000US-235077P
PR	25-SEP-2000	2000US-235082P
PR	25-SEP-2000	2000US-235134P
PR	25-SEP-2000	2000US-235280P
PR	26-SEP-2000	2000US-235637P
PR	26-SEP-2000	2000US-235638P
PR	27-SEP-2000	2000US-235711P
PR	27-SEP-2000	2000US-235720P
PR	27-SEP-2000	2000US-235840P
PR	28-SEP-2000	2000US-235636P
PR	28-SEP-2000	2000US-236028P
PR	28-SEP-2000	2000US-236032P
PR	28-SEP-2000	2000US-236033P
PR	28-SEP-2000	2000US-236034P
PR	28-SEP-2000	2000US-236109P
PR	28-SEP-2000	2000US-236111P
PR	29-SEP-2000	2000US-236642P
PR	29-SEP-2000	2000US-236691P
PR	02-OCT-2000	2000US-237172P
PR	02-OCT-2000	2000US-237173P
PR	02-OCT-2000	2000US-237278P
PR	02-OCT-2000	2000US-237294P
PR	02-OCT-2000	2000US-237295P
PR	02-OCT-2000	2000US-237316P
PR	03-OCT-2000	2000US-237425P
PR	03-OCT-2000	2000US-237598P
PR	03-OCT-2000	2000US-237604P
PR	03-OCT-2000	2000US-237606P
PR	03-OCT-2000	2000US-237608P
PR	01-NOV-2000	2000US-244867P
PR	01-NOV-2000	2000US-245084P

PA (AVAL-) AVALON PHARM.
XX
XX
Young PE, Augustus M, Carter KC, Edner R, Endress G, Horrigan S,
PI Soppet DR, Weaver Z;
XX
XX
DR WPI; 2002-188264/24.

XX Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set
XX
XX Claim 1; SEQ ID 2107; 44pp; English.

The present invention describes method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL1664 to ABL70110), or is at least 93% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytosolic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer. adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms' tumour.

Query Match	100.0%	Score 403;	DB 24;	Length 403;
Best Local Similarity	100.0%	Pred. No. 2,6e-116;		
Matches 403; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

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|||||

Db 1 TTTTTTTTTCAAAGAAACCTAGCAATTATTGATTTCTCTATTTCCAAAAAAGCAA 60

QY 61 ATACATTAGTGTATCCACACAGAAACTGGGCTGGCCGGCACAAGATTCCTGTACAAC 120

Db 61 ATACATTAGTGTATCCACACAGAAACTGGGCTGGCCGGCACAAGATTCCTGTACAAC 120

QY 121 ATGAAGCAAGGGGAAGGTGGCTACAGGGAAGCTCCAAATCCTCACAAGACCCCGG 180

Db 121 ATGAAGCAAGGGGAAGGTGGCTACAGGGAAGCTCCAAATCCTCACAAGACCCCGG 180

QY 181 TTCCTTCCTCCCTCCACCCCAAGCCGAGTCTGGTCTCTGCCACAGTTCAGCCAGATTC 240

Db 181 TTCCTTCCTCCCTCCACCCCAAGCCGAGTCTGGTCTCTGCCACAGTTCAGCCAGATTC 240

QY 241 CAAAGTGGACATGCAGACAGCAAACTGGCTCTTGGGGTCCCAAGAGGAGTGTGGAGTCA 300

Db 241 CAAAGTGGACATGCAGACAGCAAACTGGCTCTTGGGGTCCCAAGAGGAGTGTGGAGTCA 300

QY 301 GGGCTGTAGTGTGTCCCACTGCAGAGGTGGTGGTGGCCAAATAGTGATTTTGAT 360

Db 301 GGGCTGTAGTGTGTCCCACTGCAGAGGTGGTGGTGGCCAAATAGTGATTTTGAT 360

QY 361 TGGCCGCGAGACACAGAGATCCCAAGGCGAGATCTGTGTCTTT 403

Db 361 TGGCCGCGTAGACAGAGATCCCAAGGCGAGATCTGTGTCTTT 403

RESULT 2
API 66337

ID ABL66331 standard; DNA; 403 BP.

AC ABL66331
 VV

DT 15-MAY-2002 (first entry)
 YY

Lung cancer related gene sequence SEQ ID NO:4668

KW human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cytosolic; gene therapy; anti-neoplastic; Wilm's tumour; adenocarcinoma
 KW gene; ds.

OS Homo sapiens.

PN WO200194629-A2
YY

PD 13-DEC-2001.
XX

30-MAY-2001; 2001WO-0510838.
XX

PR 05-JUN-2000; 2000US-209531P.

PR 18-SEP-2000; 2000US-233617P.

PR 20-SEP-2000; 2000US-234034P.
DB 20-SEP-2000; 2000US-234034P.

PR 22-SEP-2000; 2000US-234509P.
PR 22-SEP-2000; 2000US-234567P.

PR 25-SEP-2000: 2000TS-234924B

PR	25-SEP-2000; 2000US-235082P.
FA	23-SEP-2000; 2000US-235077P.

PR 25-SEP-2000; 2000US-235280P.

PR 26-SEP-2000; 2000US-235638P.

PR 27-SEP-2000; 2000US-235720P.
DP 27-SEP-2000 200072 0000 1 00

PR 27-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-235863P.

PR 48-SEP-2000; 200005-236032P.

QY	1	TTTTTTTTTCAAAGAAACATCAGCAATTAATGATTTCTCTTTTCCAAAAAAGCA	60
Db	1	TTTTTTTTTCAAAGAAACATCAGCAATTAATGATTTCTCTTTTCCAAAAAAGCA	60
QY	61	ATACATTAGTGTATCACACAGAAACTGGGCTTGCGGCACAGTTCCTCTACAAAC	120
Db	61	ATACATTAGTGTATCACACAGAAACTGGGCTTGCGGCACAGTTCCTCTACAAAC	120
QY	121	ATCAGCAAGGGAGGTGGCTTACAGGAAAGCTCCAAAGATCCCTCACAGCAGCCCCG	180
Db	121	ATCAGCAAGGGAGGTGGCTTACAGGAAAGCTCCAAAGATCCCTCACAGCAGCCCCG	180
QY	181	TTCCCTTCCTGGCCACGCCGACGGCAGCTTGGGCTCCGACGCAAGTTCAGCCAGATTC	240
Db	181	TTCCCTTCCTGGCCACGCCGACGGCAGCTTGGGCTCCGACGCAAGTTCAGCCAGATTC	240

PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P

PR	02-OCT-2000; 2000US-237295P.
PR	02-OCT-2000; 2000US-237316P.

PR 03-OCT-2000; 2000US-237598P.

us-09-954-

PA (AVAL-) AVALON PHARM.

XX
DB WPI: 2002-188264/24.

PS Claim 1: SEO ID 6048; 44pp; English.

SO Sequence 403 BP; 98 A; 109 C; 104 G; 92 T; 0 other;

Query Match 100.0%; Score 403; DB 24; Length 403;
Best Local Similarity 100.0%; Pred. No. 2.6e-116;
Matches 403: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TTTTTTTTTTCAAAGAAACACTAGCAATTTATTGATTTTCTCTATTTCCAAAAAAGCAA	60
Db	1	TTTTTTTTTTCAAAGAAACACTAGCAATTTATTGATTTTCTCTATTTCCAAAAAAGCAA	60
Qy	61	ATACATTAGTGTATCACACAAGGAAACTGGGCCGTGGCCGGCACAAGGTTCTCTACAAAC	120
Db	61	ATACATTAGTGTATCACACAAGGAAACTGGGCCGTGGCCGGCACAAGGTTCTCTACAAAC	120
Qy	121	ATGAAGCAAGGGGAAGGTGGGCTACAGGGAAGCTCCAAGATCCCTCACAGCAGCCCCCGG	180
Db	121	ATGAAGCAAGGGGAAGGTGGGCTACAGGGAAGCTCCAAGATCCCTCACAGCAGCCCCCGG	180
Qy	181	TTCCCTTCCCTGCCACCCAGCCGAGTCTTGGTCTGCCAGCCAGTTCAGCCAGATTC	240
Db	181	TTCCCTTCCCTGCCACCCAGCCGAGTCTTGGTCTGCCAGCCAGTTCAGCCAGATTC	240
Qy	241	CAAGGTGGACATGCAGACAGCAAACTGCCTCTTGGGTCCCCAGGAGGAGTGTGGAGTCA	300
Db	241	CAAGGTGGACATGCAGACAGCAAACTGCCTCTTGGGTCCCCAGGAGGAGTGTGGAGTCA	300
Qy	301	GGGCTGCTAGTGTGGTCCCCACTGCAGAGGTGGCTGGTGGCCAACTGACTGGATTGTGCAT	360
Db	301	GGGCTGCTAGTGTGGTCCCCACTGCAGAGGTGGCTGGTGGCCAACTGACTGGATTGTGCAT	360
Qy	361	TGGCCGCTAGCACAGGAGATCCAGGGCAGAGTCTGTGTCCTT	403
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For SEA ID NO: 1247

us-09-954-1

US-09-954-1

Location/Qualifiers
1. .448

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GGAG	120	
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PAAC	180	
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AGGG	300	
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WCTT	360	
WCTT	360	
CAAT	420	
CAAT	420	
CAAT	420	

ALIGNMENTS

RESULT 1
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ID ABL63977 standard; DNA; 448 BP.
XX
AC ABL63977;
XX
DT 15-MAY-2002 (first entry)
XX
DE Breast cancer related gene sequence SEQ ID NO:2314.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US10838.
XX
PR 05-JUN-2000; 2000US-209473P.
PR 05-JUN-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234509P.
PR 22-SEP-2000; 2000US-234567P.

